CLAIMS

1. An assay for assessing the risk of disease in an individual, wherein said assay comprises the steps of;

(i) isolating a population of cells from normal tissue of said individual, and

(ii) quantitatively determining the frequency of epimutation of a particular gene in said population of cells, wherein the epimutation of said gene is associated with said disease and said gene is other than one that is subject to normal parent of origin-specific expression.

2. The assay of claim 1, wherein the normal tissue is selected from the group consisting of normal peripheral blood, normal hair follicle tissue and normal tissue from the buccal cavity.

3. The assay of claim 1, wherein the normal tissue is normal peripheral blood.

4. The assay of any one of claims 1 to 3, wherein the epimutation is DNA methylation.

5. The assay of any one of claims 1 to 4, wherein the epimutation is present in the promoter or other regulatory region of the gene and is associated with transcriptional silencing of said gene.

6. The assay of any one of claims 1 to 5, wherein the epimutation is associated with cancer.

7. The assay of any one of claims 1 to 6, wherein the epimutation is present in a tumour suppressor gene.

8. The assay of claim 7, wherein the epimutation is present in a gene selected from the group consisting of *hMLH1, hMSH2, APC 1A, APC 1B* and *p16.*

9. The assay of claim 8, wherein the epimutation is present in *hMLH1.*